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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,167

DATE: 02/21/2001

TIME: 11:03:09

Input Set : A:\ES.txt

Output Set: N:\CRF3\02212001\1744167.raw

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3 <110> APPLICANT: HSC Research and Development Limited Partnership

5 <120> TITLE OF INVENTION: SARA PROTEINS

7 <130> FILE REFERENCE: 3206-172/PAR

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/744,167

10 <141> CURRENT FILING DATE: 1999-07-20

12 <150> PRIOR APPLICATION NUMBER: 2,237,701

13 <151> PRIOR FILING DATE: 1998-07-20

15 <160> NUMBER OF SEQ ID NOS: 8

17 <170> SOFTWARE: PatentIn Ver. 2.1

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 4839

21 <212> TYPE: DNA

22 <213> ORGANISM: Homo sapiens

24 <400> SEQUENCE: 1

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26 agtctgttcc ttatcacgtg tgtaagggga aaaaggttta aacaagtctc ttaagtgggtg 120

27 tttcctcacc gatggagaat tacttccaag cagaagctt caacctggga caaggtgtta 180

28 gatgaatttg aacaaaacga agatgaaatc gtttcttcta ctttatttggta tacaatgtgg 240

29 aataagatc tagatcccc ttctcaccgg ctgtcattta accctacttt ggccagtgtg 300

30 aatqaatctg cagtttctaa tgagtccaa ccacaactga aagtcttctc cctggtctat 360

31 tcagctccc tgaccacacca ggaagaggat cactgtgtca atggacacca ctgtatctt 420

32 aatccagaga ttgccacaat gtggattgtat gaaaatgtgg ttgcagaaga ccagttattt 480

33 aagaaaaact atagttggta tgataatgc agtgctgtt aagtggaga gaagaaatgt 540

34 ggaaacctgg ttgtctgcc agatgaaatc aatgttctt ttttagccgt catgcataac 600

35 tgtgataaaa ggacattaca aaacgattt caggattgtt ataattataa tagtcaatcc 660

36 cttatggatg cttttagctg ttcaactggat aatgaaaaca gacaaactga tcaattttgt 720

37 tttatgtataa atgagtccac tgaaaaatg atgaatttca agaaacaaat ggatccattt 780

38 aatagaccgaa aacagagggtt gagatctgtt aaccatctgt gtccctacttc atctgtatgt 840

39 ctagccatgt tctgttcccc ttccacaattt aaggatgtac gaaatgttgg tagagacccc 900

40 tecatgtctg cgattacaatg tttaacgggtt gattcgttata ttcattttttt gggacacat 960

41 ggatgtctg ctgtttttttt gcaagagaac tatataccat atgaggaccc cactggccaa 1020

42 atcagctctc ctaggacaga tctagggttcc ccaaatttcc ttcccacat gagtggggg 1080

43 attttgcataaaa agaaagggcc agcagaggat agcaccactt aagaatccct ccggctctgtt 1140

44 ttacctttgc ttctcaaaacc agacatgtt aatgggttgc gaaatgttgc tgactgttgc 1200

45 cgggtttcag attgccttgtt gcttaatgtt gttgggtgtt atgaaaatgtt aggttatgtt 1260

46 catgaagaaa ctcttggcac tacagaattt cttatataatgtt cagacgtttt ctctgtatct 1320

47 caggacatgtt ctaattggaa gttgactaaa cttaaatgtt gtaatgttgc ccaagttaaac 1380

48 gaagaaaaagg aaaatgttgc acagattgtt cggctgttggg acactaatgtt tgatgttgc 1440

49 ggacagtgtt gttggattttttt gatgttgcgtt ctgtatttt aaggaaactt cattatgtt 1500

50 agtgaagaaat gtgatgttgc cactgttttata gacacaccat cagcaatattt tctatctat 1560

51 ggttgttgcattt cttatgttgc gcaagacccca ggtgtttttt ttgttccaaa gacttttaccc 1620

52 tccaaagaag attcagttttt agaagaaaaaaa gaaatgttgc gaaatgttgc agaatgttgc 1680

53 tcaaatatattt atgaaacatgtt agggaaatgtt gccacaccaatg ggtgttgcacttttaccc 1740

54 agcaactgtt gttttttttt gttttttttt ttatataatgtt ttatataatgtt agttccatca 1800

55 gtgtttttttt gatgttcccc caaggatgtt gcaagccgtt catctatgtt tgttccctttt 1860

56 ggtgttgcataaa gacccaaatgtt accttcaatgtt cttaaatgtt gttttttttt 1920

57 gaccattttttcaaaaatgtt gttttttttt ttatataatgtt gttttttttt 1980

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109 <211> LENGTH: 1323
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 2
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115 1 5 10 15
117 Asn Tyr Ser Trp Asp Asp Gln Cys Ser Ala Val Glu Val Gly Glu Lys
118 20 25 30
120 Lys Cys Gly Asn Leu Ala Cys Leu Pro Asp Glu Lys Asn Val Leu Val
121 35 40 45
123 Val Ala Val Met His Asn Cys Asp Lys Arg Thr Leu Gln Asn Asp Leu
124 50 55 60
126 Gln Asp Cys Asn Asn Tyr Asn Ser Gln Ser Leu Met Asp Ala Phe Ser
127 65 70 75 80
129 Cys Ser Leu Asp Asn Glu Asn Arg Gln Thr Asp Gln Phe Ser Phe Ser
130 85 90 95
132 Ile Asn Glu Ser Thr Glu Lys Asp Met Asn Ser Glu Lys Gln Met Asp
133 100 105 110
135 Pro Leu Asn Arg Pro Lys Thr Glu Gly Arg Ser Val Asn His Leu Cys
136 115 120 125
138 Pro Thr Ser Ser Asp Ser Leu Ala Ser Val Cys Ser Pro Ser Gln Leu
139 130 135 140
141 Lys Asp Asp Gly Ser Ile Gly Arg Asp Pro Ser Met Ser Ala Ile Thr
142 145 150 155 160
144 Ser Leu Thr Val Asp Ser Val Ile Ser Ser Gln Gly Thr Asp Gly Cys
145 165 170 175
147 Pro Ala Val Lys Lys Gln Glu Asn Tyr Ile Pro Asp Glu Asp Leu Thr
148 180 185 190
150 Gly Lys Ile Ser Ser Pro Arg Thr Asp Leu Gly Ser Pro Asn Ser Phe
151 195 200 205
153 Ser His Met Ser Glu Gly Ile Leu Met Lys Lys Glu Pro Ala Glu Glu
154 210 215 220
156 Ser Thr Thr Glu Glu Ser Leu Arg Ser Gly Leu Pro Leu Leu Lys
157 225 230 235 240
159 Pro Asp Met Pro Asn Gly Ser Gly Arg Asn Asn Asp Cys Glu Arg Cys
160 245 250 255
162 Ser Asp Cys Leu Val Pro Asn Glu Val Arg Ala Asp Glu Asn Glu Gly
163 260 265 270
165 Tyr Glu His Glu Glu Thr Leu Gly Thr Thr Glu Phe Leu Asn Met Thr
166 275 280 285
168 Glu His Phe Ser Glu Ser Gln Asp Met Thr Asn Trp Lys Leu Thr Lys
169 290 295 300
171 Leu Asn Glu Met Asn Asp Ser Gln Val Asn Glu Glu Lys Glu Lys Phe
172 305 310 315 320
174 Leu Gln Ile Ser Gln Pro Glu Asp Thr Asn Gly Asp Ser Gly Gly Gln
175 325 330 335
177 Cys Val Gly Leu Ala Asp Ala Gly Leu Asp Leu Lys Gly Thr Cys Ile
178 340 345 350
180 Ser Glu Ser Glu Glu Cys Asp Phe Ser Thr Val Ile Asp Thr Pro Ala

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181	355	360	365
183	Ala Asn Tyr Leu Ser Asn Gly Cys Asp Ser Tyr Gly Met Gln Asp Pro		
184	370	375	380
186	Gly Val Ser Phe Val Pro Lys Thr Leu Pro Ser Lys Glu Asp Ser Val		
187	385	390	395
189	400		
190	Thr Glu Glu Lys Glu Ile Glu Glu Ser Lys Ser Glu Cys Tyr Ser Asn		
192	405	410	415
193	Ile Tyr Glu Gln Arg Gly Asn Glu Ala Thr Glu Gly Ser Gly Leu Leu		
195	420	425	430
196	Leu Asn Ser Thr Gly Asp Leu Met Lys Lys Asn Tyr Leu His Asn Phe		
198	435	440	445
199	Cys Ser Gln Val Pro Ser Val Leu Gly Gln Ser Ser Pro Lys Val Val		
201	450	455	460
202	Ala Ser Leu Pro Ser Ile Ser Val Pro Phe Gly Gly Ala Arg Pro Lys		
204	465	470	475
205	480	490	495
207	Gln Pro Ser Asn Leu Lys Leu Gln Ile Pro Lys Pro Leu Ser Asp His		
210	Leu Gln Asn Asp Phe Pro Ala Asn Ser Gly Asn Asn Thr Lys Asn Lys		
211	500	505	510
213	Asn Asp Ile Leu Gly Lys Ala Lys Leu Gly Glu Asn Ser Ala Thr Asn		
214	515	520	525
216	Val Cys Ser Pro Ser Leu Gly Asn Ile Ser Asn Val Asp Thr Asn Gly		
217	530	535	540
219	Glu His Leu Glu Ser Tyr Glu Ala Glu Ile Ser Thr Arg Pro Cys Leu		
220	545	550	555
222	560		
223	Ala Leu Ala Pro Asp Ser Pro Asp Asn Asp Leu Arg Ala Gly Gln Phe		
225	565	570	575
226	Gly Ile Ser Ala Arg Lys Pro Phe Thr Thr Leu Gly Glu Val Ala Pro		
228	580	585	590
229	Val Trp Val Pro Asp Ser Gln Ala Pro Asn Cys Met Lys Cys Glu Ala		
231	595	600	605
232	Arg Phe Thr Phe Thr Lys Arg Arg His His Cys Arg Ala Cys Gly Lys		
233	610	615	620
234	Val Phe Cys Ala Ser Cys Cys Ser Leu Lys Cys Lys Leu Leu Tyr Met		
235	625	630	635
237	640		
238	Asp Arg Lys Glu Ala Arg Val Cys Val Ile Cys His Ser Val Leu Met		
239	645	650	655
240	Asn Ala Gln Ala Trp Glu Asn Met Met Ser Ala Ser Ser Gln Ser Pro		
241	660	665	670
243	Asn Pro Asn Asn Pro Ala Glu Tyr Cys Ser Thr Ile Pro Pro Leu Gln		
244	675	680	685
246	Gln Ala Gln Ala Ser Gly Ala Leu Ser Ser Pro Pro Pro Thr Val Met		
247	690	695	700
249	Val Pro Val Gly Val Leu Lys His Pro Gly Ala Glu Val Ala Gln Pro		
250	705	710	715
252	720		
253	Arg Glu Gln Arg Arg Val Trp Phe Ala Asp Gly Ile Leu Pro Asn Gly		
	725	730	735
	Glu Val Ala Asp Ala Ala Lys Leu Thr Met Asn Gly Thr Ser Ser Ala		
	740	745	750

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255 Gly Thr Leu Ala Val Ser His Asp Pro Val Lys Pro Val Thr Thr Ser
256 755 760 765
258 Pro Leu Pro Ala Glu Thr Asp Ile Cys Leu Phe Ser Gly Ser Ile Thr
259 770 775 780
261 Gln Val Gly Ser Pro Val Gly Ser Ala Met Asn Leu Ile Pro Glu Asp
262 785 790 795 800
264 Gly Leu Pro Pro Ile Leu Ile Ser Thr Gly Val Lys Gly Asp Tyr Ala
265 805 810 815
267 Val Glu Glu Lys Pro Ser Gln Ile Ser Val Met Gln Gln Leu Glu Asp
268 820 825 830
270 Gly Gly Pro Asp Pro Leu Val Phe Val Leu Asn Ala Asn Leu Leu Ser
271 835 840 845
273 Met Val Lys Ile Val Asn Tyr Val Asn Arg Lys Cys Trp Cys Phe Thr
274 850 855 860
276 Thr Lys Gly Met His Ala Val Gly Gln Ser Glu Ile Val Ile Leu Leu
277 865 870 875 880
279 Gln Cys Leu Pro Asp Glu Lys Cys Leu Pro Lys Asp Ile Phe Asn His
280 885 890 895
282 Phe Val Gln Leu Tyr Arg Asp Ala Leu Ala Gly Asn Val Val Ser Asn
283 900 905 910
285 Leu Gly His Ser Phe Phe Ser Gln Ser Phe Leu Gly Ser Lys Glu His
286 915 920 925
288 Gly Gly Phe Leu Tyr Val Thr Ser Thr Tyr Gln Ser Leu Gln Asp Leu
289 930 935 940
291 Val Leu Pro Thr Pro Pro Tyr Leu Phe Gly Ile Leu Ile Gln Lys Trp
292 945 950 955 960
294 Glu Thr Pro Trp Ala Lys Val Phe Pro Ile Arg Leu Met Leu Arg Leu
295 965 970 975
297 Gly Ala Glu Tyr Arg Leu Tyr Pro Cys Pro Leu Phe Ser Val Arg Phe
298 980 985 990
300 Arg Lys Pro Leu Phe Gly Glu Thr Gly His Thr Ile Met Asn Leu Leu
301 995 1000 1005
303 Ala Asp Phe Arg Asn Tyr Gln Tyr Thr Leu Pro Val Val Gln Gly Leu
304 1010 1015 1020
306 Val Val Asp Met Glu Val Arg Lys Thr Ser Ile Lys Ile Pro Ser Asn
307 1025 1030 1035 1040
309 Arg Tyr Asn Glu Met Met Lys Ala Met Asn Lys Ser Asn Glu His Val
310 1045 1050 1055
312 Leu Ala Gly Gly Ala Cys Phe Asn Glu Lys Ala Asp Ser His Leu Val
313 1060 1065 1070
315 Cys Val Gln Asn Asp Asp Gly Asn Tyr Gln Thr Gln Ala Ile Ser Ile
316 1075 1080 1085
318 His Asn Gln Pro Arg Lys Val Thr Gly Ala Ser Phe Phe Val Phe Ser
319 1090 1095 1100
321 Gly Ala Leu Lys Ser Ser Ser Gly Tyr Leu Ala Lys Ser Ser Ile Val
322 1105 1110 1115 1120
324 Glu Asp Gly Val Met Val Gln Ile Thr Ala Glu Asn Met Asp Ser Leu
325 1125 1130 1135
327 Arg Gln Ala Leu Arg Glu Met Lys Asp Phe Thr Ile Thr Cys Gly Lys

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number